

# SEQUENCE LISTING

(1) GENERAL INFORMATION:  
(iii) NUMBER OF SEQUENCES: 5

(2) INFORMATION FOR SEQ ID No: 1  
(i) CHARACTERISTICS OF THE SEQUENCE:

(A) LENGTH:  
(B) TYPE: nucleotide  
(C) NUMBER OF STRANDS: double  
(D) CONFIGURATION: linear

(ii) TYPE OF MOLECULE: DNA

(ix) CHARACTERISTICS

(A) NAME/KEY:

(xi) DESCRIPTION OF THE SEQUENCES: SEQ ID No: 1:

GAATTCAGAT GCCTCATACC TTGGGATTAA AAAATTGATG TTCATTGTGTT ATATATCCTG	60
GGCGGACAGG CCGGCTCGTA TTCTTCAGGG GTGTCGCCTA CCCAGTGCAC AGGAGGTCC	120
GGAGGTGTCT TGGATGGAAA GTAAGGCCAT TTGTGGGTTC TCATCCATGT CATCGTCCCT	180
TTCGGCTGTT TCACCAAGAT CCAATTATTC CTCCAGGACT TTCAACCCTC AGAATGGAAA	240
CAGAGATGAA ACTCTCTGTG CAAATCGTAG ATATCGATTG GAGACATTGA AACCACGGAG	300
TTTGAAATAA AAGTATAAAT ACCTCCGAAA ACGCAGAGTT TAAG ATG AAA GGT ATT	356
Met Lys Gly Ile	
1	
TCT AAG ATC CTC TCT GCC TCT ATT GCC CTG ATG AAG TTG GAG AAT GTC	404
Ser Lys Ile Leu Ser Ala Ser Ile Ala Leu Met Lys Leu Glu Asn Val	
5 10 15 20	
TAT TCA GCA ACC GCA CTG TGC AGC AAT GCA TAT GGC CTA ACT CCG GGA	452
Tyr Ser Ala Thr Ala Leu Cys Ser Asn Ala Tyr Gly Leu Thr Pro Gly	
25 30 35	
CAA CAG GGT ATG GCT CAG CAG CCG TCG TAT GTG CTG ATC CCC AGC ACC	500
Gln Gln Gly Met Ala Gln Gln Pro Ser Tyr Val Leu Ile Pro Ser Thr	
40 45 50	
CCG GGA ACC ATA GCA AAC TGT GCA AGC GGT TCA CAG GAC ACA TAT TCT	548
Pro Gly Thr Ile Ala Asn Cys Ala Ser Gly Ser Gln Asp Thr Tyr Ser	
55 60 65	
CCT TCT CCC GCT GCA CCC ACA TCT CCA GTG ACT CCG GGG AAA ACT AGC	596
Pro Ser Pro Ala Ala Pro Thr Ser Pro Val Thr Pro Gly Lys Thr Ser	
70 75 80	
GAG AAT GAG ACA TCT CCA TCG GCT CCT GCA GAA GAT GTA GGA ACA TGC	644
Glu Asn Glu Thr Ser Pro Ser Ala Pro Ala Glu Asp Val Gly Thr Cys	
85 90 95 100	
AAG ATT GCC GTA TTG AAG CAC TGC GAC GCA CCA GGA ACA ACA TCA GGG	692
Lys Ile Ala Val Leu Lys His Cys Asp Ala Pro Gly Thr Thr Ser Gly	
105 110 115	

0054520000





ATG AGA AGG AAC ATG ATT GAG TGC CAG AAA AGA AGC TCG GAG GCA ACA	667
Met Arg Arg Asn Met Ile Glu Cys Gln Lys Arg Ser Ser Glu Ala Thr	
55 60 65 70	
AAG GCG ATG ATT GAA AGG GCA AAT GAA AAG GCT GTA GAA TCA TTC AAC	715
Lys Ala Met Ile Glu Arg Ala Asn Glu Lys Ala Val Glu Ser Phe Asn	
75 80 85	
AAG GAA GTT AGC AAA GGA CCT AGC CAA AAG GAT GGA GGC CAG TGC ATA	763
Lys Glu Val Ser Lys Gly Pro Ser Gln Lys Asp Gly Gly Gln Cys Ile	
90 95 100	
GAA AAA GCT GTA CAA GGT ACC GAT AGG TGT ATT CTC GCT GGA ATA ATC	811
Glu Lys Ala Val Gln Gly Thr Asp Arg Cys Ile Leu Ala Gly Ile Ile	
105 110 115	
GAT AAG GCG GTG AAC AAG CGC AAG TAC AGA ATC TCA GAT GTG GAG AAC	859
Asp Lys Ala Val Asn Lys Arg Lys Tyr Arg Ile Ser Asp Val Glu Asn	
120 125 130	
AGC ACC TCG CTC TAC AGA GGA GAC AAG CTA ATT GCC CTA ATT GTC AAT	907
Ser Thr Ser Leu Tyr Arg Gly Asp Lys Leu Ile Ala Leu Ile Val Asn	
135 140 145 150	
GTC GAC TAT GGG CTG CAG CCG ATC ACT AAG CCA AAG AAG AAG AAG TCC	955
Val Asp Tyr Gly Leu Gln Pro Ile Thr Lys Pro Lys Lys Lys Lys Ser	
155 160 165	
AAG ATA ATG GCG AAT CTC CCT CAG CCG AAG AGA GAG ATG TAT TTC AAC	1003
Lys Ile Met Ala Asn Leu Pro Gln Pro Lys Arg Glu Met Tyr Phe Asn	
170 175 180	
CAA ATC GGT CAG CTT GTT GGA GCA AGA GGA ACG TTC CCC CAG GAA AAC	1051
Gln Ile Gly Gln Leu Val Gly Ala Arg Gly Thr Phe Pro Gln Glu Asn	
185 190 195	
AAG GAG GAC TGC AAG CCT TGT GAG GGT CCC AAG AAG ACT GTT GAA ACT	1099
Lys Glu Asp Cys Lys Pro Cys Glu Gly Pro Lys Lys Thr Val Glu Thr	
200 205 210	
ACT TCT GAG AAA TGT AAT CTT GGG TGC GAG CTT AAA GGA ACA TCT GCT	1147
Thr Ser Glu Lys Cys Asn Leu Gly Cys Glu Leu Lys Gly Thr Ser Ala	
215 220 225 230	
CTG ATA AGC AAG GCC ATA CAG AAG AAG GAA GTC AAG GAC ACG AAG GAA	1195
Leu Ile Ser Lys Ala Ile Gln Lys Lys Glu Val Lys Asp Thr Lys Glu	
235 240 245	
GGG GAG AAA AGT GCA AGC CAG GAC TCT GAT GGC GAG GGC ACT GCT GAG	1243
Gly Glu Lys Ser Ala Ser Gln Asp Ser Asp Gly Glu Gly Thr Ala Glu	
250 255 260	
GAT GCG GAA GTA CAG CAA CCT TCT GCG GAC GGC GAG GGT CTA GAG TAA	1291
Asp Ala Glu Val Gln Gln Pro Ser Ala Asp Gly Glu Gly Leu Glu	
265 270 275 277	
TTTTTAAATT AAAATCTCCC TGGATTGAAT CTTCAAGTGC TTTTGTGAAA GACTTTGGGA	1351
ACATTTTCGTG AAGGCTAACA TAAATTGTGA ATCTCAGGTC ACTCGATGGA ATAGTCAATT	1411
CGTATTTCTT TTCCTTGGAT GGTCTGCCCC ACCAGCCTGT TCCTGGCAGT TATCGCATCG	1471
TCGACAGAGT CAACTGAAC GAATCCATAT CCTTTGGACA TCTTCTTGTA TTGGTCGTAG	1531
ACTATTACTA CCCGATAGTT CAGTATCTCA CTGATCCTCT CCTTGAGAAG GTCTCTAACC	1591

Country	Year	Population (millions)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Urban population density (per sq km)
Algeria	1980	13.1	6.1	46.6	10.1	10.1
Algeria	1985	13.1	6.1	46.6	10.1	10.1
Algeria	1990	13.1	6.1	46.6	10.1	10.1
Algeria	1995	13.1	6.1	46.6	10.1	10.1
Algeria	2000	13.1	6.1	46.6	10.1	10.1
Algeria	2005	13.1	6.1	46.6	10.1	10.1
Algeria	2010	13.1	6.1	46.6	10.1	10.1
Algeria	2015	13.1	6.1	46.6	10.1	10.1
Algeria	2020	13.1	6.1	46.6	10.1	10.1
Algeria	2025	13.1	6.1	46.6	10.1	10.1
Algeria	2030	13.1	6.1	46.6	10.1	10.1
Algeria	2035	13.1	6.1	46.6	10.1	10.1
Algeria	2040	13.1	6.1	46.6	10.1	10.1
Algeria	2045	13.1	6.1	46.6	10.1	10.1
Algeria	2050	13.1	6.1	46.6	10.1	10.1
Algeria	2055	13.1	6.1	46.6	10.1	10.1
Algeria	2060	13.1	6.1	46.6	10.1	10.1
Algeria	2065	13.1	6.1	46.6	10.1	10.1
Algeria	2070	13.1	6.1	46.6	10.1	10.1
Algeria	2075	13.1	6.1	46.6	10.1	10.1
Algeria	2080	13.1	6.1	46.6	10.1	10.1
Algeria	2085	13.1	6.1	46.6	10.1	10.1
Algeria	2090	13.1	6.1	46.6	10.1	10.1
Algeria	2095	13.1	6.1	46.6	10.1	10.1
Algeria	2100	13.1	6.1	46.6	10.1	10.1
Algeria	2105	13.1	6.1	46.6	10.1	10.1
Algeria	2110	13.1	6.1	46.6	10.1	10.1
Algeria	2115	13.1	6.1	46.6	10.1	10.1
Algeria	2120	13.1	6.1	46.6	10.1	10.1
Algeria	2125	13.1	6.1	46.6	10.1	10.1
Algeria	2130	13.1	6.1	46.6	10.1	10.1
Algeria	2135	13.1	6.1	46.6	10.1	10.1
Algeria	2140	13.1	6.1	46.6	10.1	10.1
Algeria	2145	13.1	6.1	46.6	10.1	10.1
Algeria	2150	13.1	6.1	46.6	10.1	10.1
Algeria	2155	13.1	6.1	46.6	10.1	10.1
Algeria	2160	13.1	6.1	46.6	10.1	10.1
Algeria	2165	13.1	6.1	46.6	10.1	10.1
Algeria	2170	13.1	6.1	46.6	10.1	10.1
Algeria	2175	13.1	6.1	46.6	10.1	10.1
Algeria	2180	13.1	6.1	46.6	10.1	10.1
Algeria	2185	13.1	6.1	46.6	10.1	10.1
Algeria	2190	13.1	6.1	46.6	10.1	10.1
Algeria	2195	13.1	6.1	46.6	10.1	10.1
Algeria	2200	13.1	6.1	46.6	10.1	10.1
Algeria	2205	13.1	6.1	46.6	10.1	10.1
Algeria	2210	13.1	6.1	46.6	10.1	10.1
Algeria	2215	13.1	6.1	46.6	10.1	10.1
Algeria	2220	13.1	6.1	46.6	10.1	10.1
Algeria	2225	13.1	6.1	46.6	10.1	10.1
Algeria	2230	13.1	6.1	46.6	10.1	10.1
Algeria	2235	13.1	6.1	46.6	10.1	10.1
Algeria	2240	13.1	6.1	46.6	10.1	10.1
Algeria	2245	13.1</				

(i) CHARACTERISTICS OF THE SEQUENCE:

(B) TYPE: nucleotide

(D) CONFIGURATION: linear

### (ix) CHARACTERISTICS

(xi) DESCRIPTION OF THE SEQUENCES: SEQ ID No: 3:

ATG	AAA	GGT	ATT	TCT	AAG	GTT	CTC	TCA	GCC	TCT	ATT	GTC	CTA	ATG	AAG	48
Met	Lys	Gly	Ile	Ser	Lys	Val	Leu	Ser	Ala	Ser	Ile	Val	Leu	Met	Lys	
1				5					10					15		
TTG	AAG	GGT	GTC	TAT	TCT	ACA	ACT	GTG	CTG	TGT	GGA	GAT	TCA	ACA	CAA	96
Leu	Lys	Gly	Val	Tyr	Ser	Thr	Thr	Val	Leu	Cys	Gly	Asp	Ser	Thr	Gln	
			20					25					30			
GGA	CTG	CAG	GGC	ACA	ACC	CAA	CCG	TCA	TAT	GTG	CTG	GTT	CCT	AGT	GCA	144
Gly	Leu	Gln	Gly	Thr	Thr	Gln	Pro	Ser	Tyr	Val	Leu	Val	Pro	Ser	Ala	
			35				40					45				
CCA	GAG	ACA	ATA	GCC	AAC	TGT	GGA	TAC	AGT	CCA	CAG	AAC	ATG	TAT	GTC	192
Pro	Glu	Thr	Ile	Ala	Asn	Cys	Gly	Tyr	Ser	Pro	Gln	Asn	Met	Tyr	Val	
	50					55					60					
CCT	TCT	ACT	CCT	ACT	ACC	ATG	CCT	TCC	ACA	GTG	CCA	GGC	ACA	ACT	GGT	240
Pro	Ser	Thr	Pro	Thr	Thr	Met	Pro	Ser	Thr	Val	Pro	Gly	Thr	Thr	Gly	
65					70					75					80	
GAG	AGC	GAG	ACA	CCT	ACT	TCT	CCA	ACA	TCA	TCT	CCT	ACA	GAG	GAT	GTG	288
Glu	Ser	Glu	Thr	Pro	Thr	Ser	Pro	Thr	Ser	Ser	Pro	Thr	Glu	Asp	Val	
				85					90					95		
GGA	ACA	TGC	AAG	ATT	GCT	GTT	GTA	AAG	CAT	TGT	GAT	GCA	CCA	GGA	ACA	336
Gly	Thr	Cys	Lys	Ile	Ala	Val	Val	Lys	His	Cys	Asp	Ala	Pro	Gly	Thr	
			100					105					110			
TCA	TCA	ACA	CCT	TGC	GAA	CCG	GAA	CAG	ACT	TTG	GCC	CCC	TCT	CAG	CCA	384
Ser	Ser	Thr	Pro	Cys	Glu	Pro	Glu	Gln	Thr	Leu	Ala	Pro	Ser	Gln	Pro	
			115					120				125				
GTA	GCA	GCT	ACA	ATT	GCC	ACA	CCA	CTG	GTT	GTT	GCT	TCT	GTG	CAG	ACG	432
Val	Ala	Ala	Thr	Ile	Ala	Thr	Pro	Leu	Val	Val	Ala	Ser	Val	Gln	Thr	
			130				135					140				
CCG	CAA	GCA	GCT	GTT	ACC	ATC	CTT	ACT	CCA	AAG	GCC	GTC	TCT	GCC	CAG	480
Pro	Gln	Ala	Ala	Val	Thr	Ile	Leu	Thr	Pro	Lys	Ala	Val	Ser	Ala	Gln	
145					150					155					160	

CCG GCA ACC ATC ATT TCA TTC AAC CAG GCA CCA GGC TAC AAT	528
Pro Ala Thr Ile Ile Ser Pro Phe Asn Gln Ala Pro Gly Tyr Tyr Asn	
165 170 175	
AGT GCA ATT CCC GGG CAA ATA CTT ACA GGT AAT GTT CTC TCT CCA AGT	576
Ser Ala Ile Pro Gly Gln Ile Leu Thr Gly Asn Val Leu Ser Pro Ser	
180 185 190	
GCC TCT TCT TGC CAA GTG GTG CCC GGA ACA ACA GGA AGC TCC ACC CCC	624
Ala Ser Ser Cys Gln Val Val Pro Gly Thr Thr Gly Ser Ser Thr Pro	
195 200 205	
CAG CAG CTA CCA GGC GCT GTT TCA TCT GGA ACC ATT CCT TGC CAA ATA	672
Gln Gln Leu Pro Gly Ala Val Ser Ser Gly Thr Ile Pro Cys Gln Ile	
210 215 220	
GTA CAG GGA ACT CAA AGT AGC GGA AAC ACC CCT GGA CAG CAA TTC TTG	720
Val Gln Gly Thr Gln Ser Ser Gly Asn Thr Pro Gly Gln Gln Phe Leu	
225 230 235 240	
CCG GGA ATC GTT CCT GTT GGA AGC CTC CAG CCG GAT CAA GCT ACT TCT	768
Pro Gly Ile Val Pro Val Gly Ser Leu Gln Pro Asp Gln Ala Thr Ser	
245 250 255	
GGA ACC CCT ACC CCT TCT GTT AGC CAA AGC CAA TCT GGA CAG CAA TGC	816
Gly Thr Pro Thr Pro Ser Val Ser Gln Ser Gln Ser Gly Gln Gln Cys	
260 265 270	
TGC TGC ACT CCT CCA ATC ACA AAC CCT GTA ATG CCA ACT CCT ATG GGT	864
Cys Cys Thr Pro Pro Ile Thr Asn Pro Val Met Pro Thr Pro Met Gly	
275 280 285	
ATC AGC AGT AAT GGG TAT CCC AGC TCA ACT GCG TAC GCC CCA ACC CTT	912
Ile Ser Ser Asn Gly Tyr Pro Ser Ser Thr Ala Tyr Ala Pro Thr Leu	
290 295 300	
GGA CAA TTG GGA CCT TGC ATC GAC ACA CAG AAG TCA ACA TCA TCC TGC	960
Gly Gln Leu Gly Pro Cys Ile Asp Thr Gln Lys Ser Thr Ser Ser Cys	
305 310 315 320	
GAA CCA AAA GAA AAG CCT GTA GCA CAG TAT GGA ATG GAA GCA TGC GCT	1008
Glu Pro Lys Glu Lys Pro Val Ala Gln Tyr Gly Met Glu Ala Cys Ala	
325 330 335	
GCA CCA ACT CCA ACT GCT GTT CTA GGA AAT GCT GAG TAT CTC CTT AGC	1056
Ala Pro Thr Pro Thr Ala Val Leu Gly Asn Ala Glu Tyr Leu Leu Ser	
340 345 350	
CCG GGG ATG TAT AAT TCA CTC AAC TCT CCA TGC AAC GCT TGC TGC CAA	1104
Pro Gly Met Tyr Asn Ser Leu Asn Ser Pro Cys Asn Ala Cys Cys Gln	
355 360 365	
CAA CAA TGC TAG	1116
Gln Gln Cys *	
370 371	

(2) INFORMATION FOR SEQ ID No: 4

(i) CHARACTERISTICS OF THE SEQUENCE:

(A) LENGTH:

(B) TYPE: nucleotide

(C) NUMBER OF STRANDS: double

1. The first group of people who are not in the majority are the "minority" group. This group is made up of people who are not in the majority, but who are still in the majority. This group is made up of people who are not in the majority, but who are still in the majority.

ATG	TTG	TTA	CTT	CTC	TCA	GCA	GTT	GCT	TTT	GTT	AGC	GCT	ACA	GCA	GTC	48
Met	Leu	Leu	Leu	Leu	Ser	Ala	Val	Ala	Phe	Val	Ser	Ala	Thr	Ala	Val	
1				5					10					15		
CAG	TCA	GGT	GTT	GTC	TCC	CAG	CCT	ACA	ACA	CCC	ATT	CCG	ATT	CTT	CCT	96
Gln	Ser	Gly	Val	Val	Ser	Gln	Pro	Thr	Thr	Pro	Ile	Pro	Ile	Leu	Pro	
			20					25					30			
GGA	CAG	CCG	ATG	GGG	GGC	ATG	GCC	AAC	GGG	TGC	ACT	AAC	AAG	AAA	CTA	144
Gly	Gln	Pro	Met	Gly	Gly	Met	Ala	Asn	Gly	Cys	Thr	Asn	Lys	Lys	Leu	
		35					40					45				
GAT	GGT	GTT	GAA	ATA	ATG	AGA	AGG	AAC	ATG	GTG	GAA	TGC	CAG	AAG	AGA	192
Asp	Gly	Val	Glu	Ile	Met	Arg	Arg	Asn	Met	Val	Glu	Cys	Gln	Lys	Arg	
	50					55					60					
AAT	GCA	GAG	GCA	ACA	AAA	GCA	ATG	GTT	GAA	AGG	GCT	AAT	GAA	AAG	GCT	240
Asn	Ala	Glu	Ala	Thr	Lys	Ala	Met	Val	Glu	Arg	Ala	Asn	Glu	Lys	Ala	
65					70				75						80	
GTA	GAA	ACA	TTC	AAT	AAG	GAG	GTC	AGT	AAA	GGA	CCT	CAA	AAG	GAA	AGC	288
Val	Glu	Thr	Phe	Asn	Lys	Glu	Val	Ser	Lys	Gly	Pro	Gln	Lys	Glu	Ser	
				85					90					95		
GGC	CAG	TGC	ATA	GAA	AAA	GCT	GTA	CAG	GGC	ACC	GAC	AGA	TGT	ATT	CTT	336
Gly	Gln	Cys	Ile	Glu	Lys	Ala	Val	Gln	Gly	Thr	Asp	Arg	Cys	Ile	Leu	
			100					105					110			
GCA	GGA	ATA	ATT	GAT	AAG	GCT	GTG	AAC	AAG	CGT	AAG	TAC	AGA	ATC	TCG	384
Ala	Gly	Ile	Ile	Asp	Lys	Ala	Val	Asn	Lys	Arg	Lys	Tyr	Arg	Ile	Ser	
			115				120					125				
GAT	GTG	GAG	AAT	AGC	ACC	TCG	CTC	TAT	AGA	GGC	GAC	AAA	CTA	ATT	GCT	432
Asp	Val	Glu	Asn	Ser	Thr	Ser	Leu	Tyr	Arg	Gly	Asp	Lys	Leu	Ile	Ala	
	130					135					140					
CTA	ATT	GTC	AAT	GTT	GAC	TAT	GGA	CTT	CAG	CCA	ATT	ATC	AAA	CCA	AAG	480
Leu	Ile	Val	Asn	Val	Asp	Tyr	Gly	Leu	Gln	Pro	Ile	Ile	Lys	Pro	Lys	
145					150				155					160		
AAG	AAG	AAA	TCC	AAG	ATA	ATG	GCA	AAT	CTT	CCT	CAA	CCA	AAG	AGA	GAG	528
Lys	Lys	Lys	Ser	Lys	Ile	Met	Ala	Asn	Leu	Pro	Gln	Pro	Lys	Arg	Glu	
				165					170					175		
ATG	TAT	TTC	AAC	CAG	ATC	GGA	CAG	CTT	GTT	GGA	GCA	AAG	GGA	ACA	TTC	576
Met	Tyr	Phe	Asn	Gln	Ile	Gly	Gln	Leu	Val	Gly	Ala	Lys	Gly	Thr	Phe	
			180					185					190			
CCT	CAA	GAC	AAC	AAG	GAT	GAA	TGC	AAG	CCA	TGC	GAA	CCT	AAG	AAG	ACT	624
Pro	Gln	Asp	Asn	Lys	Asp	Glu	Cys	Lys	Pro	Cys	Glu	Pro	Lys	Lys	Thr	
		195					200					205				
GTT	GAA	ACT	GCT	TCT	GAA	AGA	TGT	AAT	CTT	GGG	TGC					





[illegible]